

SEQUENCE LISTING

INS. A4 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2107  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGGAG ACTTTTTTTT GAAAGGAAAC TAGGGAGGGA GGGAGAGGGA	60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG	115
	Met 1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT	163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His	
5 10 15	
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA	211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr	
20 25 30	
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG	259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys	
35 40 45	
TAC GGC TAC CTT CCA CCG ACT AGC CCC AGA ATG TCA GTC GTG CGC TCT	307
Tyr Gly Tyr Leu Pro Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser	
50 55 60 65	
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC	355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly	
70 75 80	
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT CAC TGG ATG AAG	403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys	
85 90 95	
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT	451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe	
100 105 110	
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC	499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His	
115 120 125	

002212 20040260

AA

AAG Lys 130	CAC His	ATC Ile	ACT Thr	TAC Tyr	AGT Ser 135	ATA Ile	AAG Lys	ASN Asn	GTA Val	ACT Thr 140	CCA Pro	AAA Lys	GTA Val	GGA Gly	GAC Asp 145	547
CCT Pro	GAG Glu	ACT Thr	CGT Arg	AAA Lys 150	GCT Ala	ATT Ile	CGC Arg	CGT Arg	GCC Ala 155	TTT Phe	GAT Asp	GTG Val	TGG Trp	CAG Gln 160	AAT Asn	595
GTA Val	ACT Thr	CCT Pro	CTG Leu 165	ACA Thr	TTT Phe	GAA Glu	GAA Glu	GTG Val 170	CCC Pro	TAC Tyr	AGT Ser	GAA Glu	TTA Leu 175	GAA Glu	AAT Asn	643
GGC Gly	AAA Lys 180	CGT Arg	GAT Asp	GTG Val	GAT Asp	ATA Ile	CCC Pro 185	ATT Ile	ATT Ile	TTT Phe	GCA Ala	TCT Ser 190	GGT Gly	TTC Phe	CAT His	691
GGG Gly 195	GAC Asp	AGC Ser	TCT Ser	CCC Pro	TTT Phe	GAT Asp 200	GGA Gly	GAG Glu	GGA Gly	GGA Gly	TTT Phe 205	TTG Leu	GCA Ala	CAT His	GCC Ala	739
TAC Tyr 210	TTC Phe	CCT Pro	GGA Gly	CCA Pro	GGA Gly 215	ATT Ile	GGA Gly	GGA Gly	GAT Asp	ACC Thr 220	CAT His	TTT Phe	GAC Asp	TCA Ser	GAT Asp 225	787
GAG Glu	CCA Pro	TGG Trp	ACA Thr	CTA Leu 230	GGA Gly	AAT Asn	CCT Pro	AAT Asn	CAT His 235	GAT Asp	GGA Gly	AAT Asn	GAC Asp	TTA Leu 240	TTT Phe	835
CTT Leu	GTA Val	GCA Ala	GTC Val 245	CAT His	GAA Glu	CTG Leu	GGA Gly	CAT His 250	GCT Ala	CTG Leu	GGA Gly	TTG Leu	GAG Glu 255	CAT His	TCC Ser	883
AAT Asn	GAC Asp	CCC Pro 260	ACT Thr	GCC Ala	ATC Ile	ATG Met	GCT Ala 265	CCA Pro	TTT Phe	TAC Tyr	CAG Gln	TAC Tyr 270	ATG Met	GAA Glu	CAG Gln	931
ACA Thr 275	CTT Leu	CAA Gln	CTA Leu	CCT Pro	AAT Asn	GAT Asp 280	GAT Asp	TAC Tyr	AGG Arg	GAT His	CAG Gln 285	AGA Arg	TAT Tyr	ATG Met	TCA Ser	979
CCT Pro 290	GAC Asp	AAG Lys	ATT Ile	CCT Pro	CCA Pro 295	CCT Pro	ACA Thr	AGA Arg	CCT Pro	CTA Leu 300	CCG Pro	ACA Thr	GTG Val	CCC Pro	CCA Pro 305	1027
CAC His	CGC Arg	TCT Ser	ATT Ile	CCT Pro 310	CCG Pro	GCT Ala	GAC Asp	CCA Pro	AGG Arg 315	AAA Lys	AAT Asn	GAC Asp	AGG Arg	CCA Pro 320	AAA Lys	1075
CCT Pro	CCT Pro	CGG Arg	CCT Pro 325	CCA Pro	ACC Thr	GGC Gly	AGA Arg	CCC Pro 330	TCC Ser	TAT Tyr	CCC Pro	GGA Gly	GCC Ala 335	AAA Lys	CCC Pro	1123
AAC Asn	ATC Ile	TGT Cys 340	GAT Asp	GGG Gly	AAC Asn	TTT Phe	AAC Asn 345	ACT Thr	CTA Leu	GCT Ala	ATT Ile	CTT Leu 350	CGT Arg	CGT Arg	GAG Glu	1171

ATG	TTT	GTT	TTC	AAG	GAC	CAG	TGG	TTT	TGG	CGA	GTG	AGA	AAC	AAC	AGG	1219
Met	Phe	Val	Phe	Lys	Asp	Gln	Trp	Phe	Trp	Arg	Val	Arg	Asn	Asn	Arg	
355						360					365					
GTG	ATG	GAT	GGA	TAC	CCA	ATG	CAA	ATT	ACT	TAC	TTC	TGG	CGG	GGC	TTG	1267
Val	Met	Asp	Gly	Tyr	Pro	Met	Gln	Ile	Thr	Tyr	Phe	Trp	Arg	Gly	Leu	
370					375					380					385	
CCT	CCT	AGT	ATC	GAT	GCA	GTT	TAT	GAA	AAT	AGC	GAC	GGG	AAT	TTT	GTG	1315
Pro	Pro	Ser	Ile	Asp	Ala	Val	Tyr	Glu	Asn	Ser	Asp	Gly	Asn	Phe	Val	
				390					395					400		
TTC	TTT	AAA	GGT	AAC	AAA	TAT	TGG	GTG	TTC	AAG	GAT	ACA	ACT	CTT	CAA	1363
Phe	Phe	Lys	Gly	Asn	Lys	Tyr	Trp	Val	Phe	Lys	Asp	Thr	Thr	Leu	Gln	
			405					410					415			
CCT	GGT	TAC	CCT	CAT	GAC	TTG	ATA	ACC	CTT	GGA	AGT	GGA	ATT	CCC	CCT	1411
Pro	Gly	Tyr	Pro	His	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Gly	Ile	Pro	Pro	
		420					425					430				
CAT	GGT	ATT	GAT	TCA	GCC	ATT	TGG	TGG	GAG	GAC	GTC	GGG	AAA	ACC	TAT	1459
His	Gly	Ile	Asp	Ser	Ala	Ile	Trp	Trp	Glu	Asp	Val	Gly	Lys	Thr	Tyr	
	435					440					445					
TTC	TTC	AAG	GGA	GAC	AGA	TAT	TGG	AGA	TAT	AGT	GAA	GAA	ATG	AAA	ACA	1507
Phe	Phe	Lys	Gly	Asp	Arg	Tyr	Trp	Arg	Tyr	Ser	Glu	Glu	Met	Lys	Thr	
450					455					460					465	
ATG	GAC	CCT	GGC	TAT	CCC	AAG	CCA	ATC	ACA	GTC	TGG	AAA	GGG	ATC	CCT	1555
Met	Asp	Pro	Gly	Tyr	Pro	Lys	Pro	Ile	Thr	Val	Trp	Lys	Gly	Ile	Pro	
				470					475					480		
GAA	TCT	CCT	CAG	GGA	GCA	TTT	GTA	CAC	AAA	GAA	AAT	GGC	TTT	ACG	TAT	1603
Glu	Ser	Pro	Gln	Gly	Ala	Phe	Val	His	Lys	Glu	Asn	Gly	Phe	Thr	Tyr	
			485					490					495			
TTC	TAC	AAG	GAA	GGA	GTA	TTG	GAA	ATT	CAA	ACA	ACC	AGA	TAC	TCA	AGG	1651
Phe	Tyr	Lys	Glu	Gly	Val	Leu	Glu	Ile	Gln	Thr	Thr	Arg	Tyr	Ser	Arg	
		500					505					510				
CTA	GAA	CCT	GGA	CAT	CCA	AGA	TCC	ATC	CTC	AAG	GAT	TTA	TCG	GGC	TGT	1699
Leu	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp	Leu	Ser	Gly	Cys	
	515					520					525					
GAT	GGA	CCA	ACA	GAC	AGA	GTT	AAA	GAA	GGA	CAC	AGC	CCA	CCA	GAT	GAT	1747
Asp	Gly	Pro	Thr	Asp	Arg	Val	Lys	Glu	Gly	His	Ser	Pro	Pro	Asp	Asp	
530					535					540					545	
GTA	GAC	ATT	GTC	ATC	AAA	CTG	GAC	AAC	ACA	GCC	AGC	ACT	GTG	AAA	GCC	1795
Val	Asp	Ile	Val	Ile	Lys	Leu	Asp	Asn	Thr	Ala	Ser	Thr	Val	Lys	Ala	
				550					555					560		
ATA	GCT	ATT	GTC	ATT	CCC	TGC	ATC	TTG	GCC							

Asp Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln  
 145 150 155 160  
 Asn Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu  
 165 170 175  
 Asn Gly Lys Arg Asp Val Asp Ile Pro Ile Ile Phe Ala Ser Gly Phe  
 180 185 190  
 His Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His  
 195 200 205  
 Ala Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser  
 210 215 220  
 Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu  
 225 230 235 240  
 Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His  
 245 250 255  
 Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu  
 260 265 270  
 Gln Thr Leu Gln Leu Pro Asn Asp Asp Tyr Arg His Gln Arg Tyr Met  
 275 280 285  
 Ser Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr Val Pro  
 290 295 300  
 Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp Arg Pro  
 305 310 315 320  
 Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly Ala Lys  
 325 330 335  
 Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu Arg Arg  
 340 345 350  
 Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg Asn Asn  
 355 360 365  
 Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp Arg Gly  
 370 375 380  
 Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly Asn Phe  
 375 390 395 400  
 Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp Thr Thr Leu  
 405 410 415  
 Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser Gly Ile Pro  
 420 425 430  
 Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val Gly Lys Thr  
 435 440 445

09734002-121200

AA  
Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu Glu Met Lys  
450 455 460  
Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp Lys Gly Ile  
455 470 475 480  
Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn Gly Phe Thr  
485 490 495  
Tyr Phe Tyr Lys Glu Gly Val Leu Glu Ile Gln Thr Thr Arg Tyr Ser  
500 505 510  
Arg Leu Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp Leu Ser Gly  
515 520 525  
Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser Pro Pro Asp  
530 535 540  
Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser Thr Val Lys  
545 550 555 560  
Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu Leu Val  
565 570 575  
Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro Arg His  
580 585 590  
Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val  
595 600 604

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

SGNVVNGCWG AYATMRTSAT

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

A4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

YTCRTSNTCR TCRAARTGRR HRTCYYC

27

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln  
1 5 10 15

Ser Ala  
18

00734002 121200

~~A4~~ (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: Amino acid

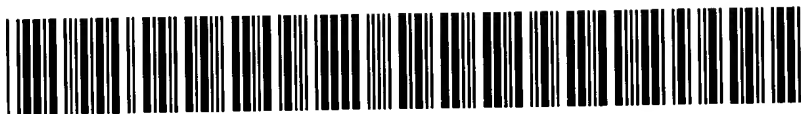
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu  
1 5 10 14

002121 20040260



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